SCORE Search Results Details for Application 10529592 and Search Result 20090427_122905_us-10-529-592a-1.rng.

This page gives you Search Results detail for the Application 10529592 and Search Result 20090427_122905_us-10-529-592a-1.rng.

Go Back to previous page

GenCore version 6.3

OM nucleic - nucleic search, using sw model

Run on: April 28, 2009, 04:12:15 ; Search time 229 Seconds
(without alignments)
63759.541 Million cell updates/sec

Title: US-10-529-592A-1
Perfect score: 881
Sequence: 1 gggccatgacccccgctgct.....aaataaagatcctctgtaac 881

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 14112681 seqs, 8286569208 residues

Total number of hits satisfying chosen parameters: 28225362

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_200812:*
1: geneseqn1:*
2: geneseqn2:*
3: geneseqn3:*
4: geneseqn4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	881	100.0	881	2	ADM96967	Adm96967 Human pan
	2	881	100.0	881	3	AES72471	Aes72471 Human C19
	3	827	93.9	893	2	ADM96969	Adm96969 Human pan
	4	827	93.9	893	3	AES72473	Aes72473 Human C19
	5	703.2	79.8	761	1	AAK88446	Aak88446 Human dig
c	6	694.2	78.8	963	1	AAI90742	Aai90742 Human pol
c	7	694.2	78.8	963	1	ADE09694	Ade09694 Novel DNA
	8	694.2	78.8	1239	3	ARC01157	Arc01157 DNA fragm
	9	692.6	78.6	1261	4	AQD66153	Aqd66153 Human chr
c	10	611	69.4	614	2	ADR26670	Adr26670 Breast ca
	11	549	62.3	2798	1	AAK90422	Aak90422 Human dig
	12	547.4	62.1	2804	1	AAK90423	Aak90423 Human dig
	13	367	41.7	574	1	ABL65256	Abl65256 Lung canc
	14	206.4	23.4	1617	1	ADE07493	Ade07493 Novel cod
	15	203	23.0	203	1	AFS82561	Afs82561 Human tra
	16	193	21.9	195	3	AQC97274	Aqc97274 Human nuc
	17	193	21.9	195	3	AQC91488	Aqc91488 Human nuc
	18	147.2	16.7	550	2	ACH77410	Ach77410 Human gen
	19	144	16.3	170	2	ACH91110	Ach91110 Human gen
	20	105.4	12.0	2721	1	ABS61407	Abs61407 Prostate
	21	75.4	8.6	763	1	ABQ27175	Abq27175 Oligonucl
c	22	75.4	8.6	763	1	ABQ27174	Abq27174 Oligonucl
	23	49.8	5.7	2000	1	ADA71938	Ada71938 Rice gene
	24	49.8	5.7	2000	3	AJG11665	Ajg11665 Rice infe
	25	49.2	5.6	2441	2	AQD19538	Aqd19538 Rice cDNA
c	26	49	5.6	763	1	ABQ27177	Abq27177 Oligonucl
	27	49	5.6	763	1	ABQ27176	Abq27176 Oligonucl
	28	48.4	5.5	852	4	AQY74734	Aqy74734 Streptomy
c	29	48.4	5.5	110000	4	AQY71306_42	Continuation (43 o
c	30	47.2	5.4	1501	3	AOB79884	Aob79884 Rice geno
c	31	47.2	5.4	88445	3	AOC17251	Aoc17251 Rice geno
c	32	47.2	5.4	88445	4	ASR04844	Asr04844 Rice geno
c	33	47.2	5.4	88805	3	AQD74525	Aqd74525 Rice geno
c	34	47	5.3	1140	1	ADB72831	Adb72831 Human LFN
c	35	47	5.3	1140	1	ADB72832	Adb72832 Human LFN
c	36	47	5.3	1140	1	ADA66377	Ada66377 Human LFN
c	37	47	5.3	1140	1	ADA66378	Ada66378 Human LFN
c	38	47	5.3	1140	1	ADA03094	Ada03094 Human LFN
c	39	47	5.3	1140	1	ADA03093	Ada03093 Human LFN
c	40	47	5.3	1140	1	ADL27172	Adl27172 Human cod
c	41	47	5.3	1377	2	ADZ12748	Adz12748 Human can
c	42	47	5.3	1545	1	AAV41906	Aav41906 Nucleotid
c	43	47	5.3	3025	2	ADZ12756	Adz12756 Human can

c	44	47	5.3	3142	4	ATN14791	Atn14791 Human tra
c	45	47	5.3	29040	1	ADL27170	Adl27170 Human gen

ALIGNMENTS

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RESULT 1
ADM96967
ID   ADM96967 standard; cDNA; 881 BP.
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AC   ADM96967;
XX
DT   01-JUL-2004  (first entry)
XX
DE   Human pancreatic cancer upregulated gene C1958V1.
XX
KW   ds; gene; cytostatic; gene therapy; pancreatic cancer; diagnosis;
KW   anti-tumor immunity.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             163. .393
FT                   /*tag=  a
FT                   /product= "C1958V1 protein"
XX
PN   WO2004031411-A2.
XX
PD   15-APR-2004.
XX
PF   12-SEP-2003; 2003WO-JP011713.
XX
PR   30-SEP-2002; 2002US-0414872P.
PR   28-FEB-2003; 2003US-0450889P.
XX
PA   (ONCO-) ONCOTHERAPY SCI INC.
PA   (UYTY ) UNIV TOKYO.
XX
PI   Nakamura Y,  Katagiri T;
XX
DR   WPI; 2004-330204/30.
DR   P-PSDB; ADM96968.
XX
PT   New C1958V1 or C1958V2 polypeptides, useful in useful in diagnosing and
PT   treating pancreatic cancer and in inducing anti tumor immunity.
XX
PS   Claim 2; SEQ ID NO 1; 71pp; English.
XX
```

CC The invention relates to the isolation of novel genes upregulated in
CC pancreatic cancer designated C1958V1 and C1958V2, their encoded
CC polypeptides (I), a sequence in which one or more amino acids are
CC substituted, deleted, inserted, and/or added and that has a biological
CC activity equivalent to the C1958V1 or C1958V2 proteins; or a sequence
CC encoded by a polynucleotide that hybridizes under stringent conditions to
CC the C1958V1 or C1958V2 polynucleotides. The polypeptides and
CC polynucleotides, compounds and compositions are useful in diagnosing and
CC treating pancreatic cancer and in inducing anti tumor immunity. This
CC sequence represents the C1958V1 cDNA sequence.
XX
SQ Sequence 881 BP; 178 A; 276 C; 264 G; 163 T; 0 U; 0 Other;

Query Match 100.0%; Score 881; DB 2; Length 881;
Best Local Similarity 100.0%; Pred. No. 2.5e-206;
Matches 881; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GGGCCATGACCCCCGCTGCTCTGTCTTGCAGGCTCGTCGCCGCGGCCCCCCGAGCCCGAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGGCCATGACCCCCGCTGCTCTGTCTTGCAGGCTCGTCGCCGCGGCCCCCCGAGCCCGAC 60

Qy         61 CGCCGCCGCCACCACCACCAGCGCCCGGGCGGGCCTCGCGCGCCTCGGGCGCGGCTCCGC 120
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Db         61 CGCCGCCGCCACCACCACCAGCGCCCGGGCGGGCCTCGCGCGCCTCGGGCGCGGCTCCGC 120

Qy        121 AGTGAGCCCACCAAGAAGGAAGCGGCCTGCAGAGGTGCCGACATGGGGCTTAAGATGTCC 180
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Qy        241 GTCCTGAACGACAAGCACCTGGACGTGCCCGACATCATCATCACGCCCCCCACCCCCACG 300
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Qy        421 CTCCTGCTCCAGCGGCCCGGCTTCAGGTGTCCGGGGGCGTGGCTGCCTGGAGCAGGTGTG 480
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Db        421 CTCCTGCTCCAGCGGCCCGGCTTCAGGTGTCCGGGGGCGTGGCTGCCTGGAGCAGGTGTG 480
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Qy        481 CTGAATACCCTGGATGGGAACTGAGCGAACCCGGGCCTCCGCTCAGAGAGACGTGGCAGG 540
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Qy        601 GACCGGACCTCTGACACCTCCAGGTTCTTGCTGACTCCGGCCTGGTGAAAGGGAGCGCCA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GACCGGACCTCTGACACCTCCAGGTTCTTGCTGACTCCGGCCTGGTGAAAGGGAGCGCCA 660

Qy        661 TGGTCCTGGCTGTTGGGGTCCCAGGGAGAGGCTCTCTTCTGGACAAACACACCCTCCCAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TGGTCCTGGCTGTTGGGGTCCCAGGGAGAGGCTCTCTTCTGGACAAACACACCCTCCCAG 720

Qy        721 CCCCCAGGGCTGTGCAAACACATGCCCCTGCCATAAGCACCAACAAGAACTTCTTGCAGG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CCCCCAGGGCTGTGCAAACACATGCCCCTGCCATAAGCACCAACAAGAACTTCTTGCAGG 780

Qy        781 TGGAGTGGCTGTTTTTTATAAGTTGTTTTACAGATACGGAAACAGTCCAAAATGGGATTT 840
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Db        781 TGGAGTGGCTGTTTTTTATAAGTTGTTTTACAGATACGGAAACAGTCCAAAATGGGATTT 840

Qy        841 ATAATTTCTTTTTTGCATTATAAATAAAGATCCTCTGTAAC 881
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Db        841 ATAATTTCTTTTTTGCATTATAAATAAAGATCCTCTGTAAC 881
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RESULT 2
AES72471
ID   AES72471 standard; cDNA; 881 BP.
XX
AC   AES72471;
XX
DT   03-MAY-2007  (first entry)
XX
DE   Human C1958 splice  variant 1, cDNA.
XX
KW   Pancreatic ductal adenocarcinoma; cancer; cytostatic; tumor marker;
KW   protein therapy; screening; splice variant; ss; gene; C1958V1; apoptosis;
KW   gene therapy; pancreas tumor; lung tumor; renal tumor; testicle tumor.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             163. .393
FT                   /*tag=  a
FT                   /product= "C1958V1 protein"
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XX
PN WO2007013358-A2.
XX
PD 01-FEB-2007.
XX
PF 14-JUL-2006; 2006WO-JP314442.
XX
PR 28-JUL-2005; 2005US-0703791P.
XX
PA (ONCO-) ONCOTHERAPY SCI INC.
PA (UYTY) UNIV TOKYO.
XX
PI Nakamura Y, Katagiri T, Inaki K;
XX
DR WPI; 2007-283242/27.
DR P-PSDB; AES72472.
XX
PT New VIVIT polypeptide useful for treating or preventing cancer, such as
PT pancreatic cancer, lung cancer, kidney cancer and testicular tumor.
XX
PS Disclosure; SEQ ID NO 1; 78pp; English.
XX
CC The invention relates to a VIVIT polypeptide (AES72497) and at least a
CC fragment of the human C1958 sequence appearing as AES72472, in which
CC residues at positions 37-41 is replaced with AES72497, or an amino acid
CC sequence of a polypeptide functionally equivalent to the polypeptide
CC comprising the fragment sequence. Also included are an agent for
CC treating/preventing cancer (comprising as an active ingredient the VIVIT
CC polypeptide, or a polynucleotide encoding the polypeptide), a
CC pharmaceutical composition (comprising the VIVIT polypeptide, and a
CC carrier), screening (M1) for a compound useful in treating/preventing
CC cancers (involving (a) contacting a polypeptide comprising a PPP3CA-
CC binding domain of a C1958 polypeptide with a polypeptide comprising a
CC C1958-binding domain of a PPP3CA polypeptide in the presence of a test
CC compound, (b) detecting binding between the polypeptides, and (c)
CC selecting a test compound that inhibits binding between the
CC polypeptides), a kit for screening for a compound for treating or
CC preventing cancers, treating/preventing cancers in a subject (involving
CC administering the compound selected above), and inducing apoptosis in a
CC cell (involving introducing a polypeptide having a dominant-negative
CC effect against C1958 or a polynucleotide encoding the polypeptide into
CC the cell, where the polypeptide comprises a fragment sequence having
CC AES72497, or the mutated C1958 above). The polypeptide is modified with a
CC cell-membrane permeable substance, which has the general formula [R]-[D],
CC where [R] represents the cell-membrane permeable substance, and [D]
CC represents the amino acid sequence of a fragment sequence of AES72497, or
CC the mutated C1958 peptide. The VIVIT polypeptide is useful for treating
CC and/or preventing cancer, preferably pancreatic cancer (especially
CC Pancreatic ductal adenocarcinoma), lung cancer, kidney cancer and

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CC   testicular tumor. (M1) is useful for screening a compound for treating or
CC   preventing cancers. The present sequence encodes a splice variant of
CC   human C1958.
XX
SQ   Sequence 881 BP; 178 A; 276 C; 264 G; 163 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 881;  DB 3;  Length 881;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-206;
  Matches  881;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy        121 AGTGAGCCCACCAAGAAGGAAGCGGCCTGCAGAGGTGCCGACATGGGGCTTAAGATGTCC 180
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Qy        361 CCAGATGATGGAGAAATCGACCCAGAAGCCTGAGGAGGTGTCCTGGGTTTGGCTGGCTGG 420
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Qy        421 CTCCTGCTCCAGCGGCCCGGCTTCAGGTGTCCGGGGGCGTGGCTGCCTGGAGCAGGTGTG 480
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Qy        601 GACCGGACCTCTGACACCTCCAGGTTCTTGCTGACTCCGGCCTGGTGAAAGGGAGCGCCA 660
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Qy        781 TGGAGTGGCTGTTTTTTATAAGTTGTTTTACAGATACGGAAACAGTCCAAAATGGGATTT 840
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Db        841 ATAATTTCTTTTTTGCATTATAAATAAAGATCCTCTGTAAC 881
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RESULT 3
ADM96969
ID   ADM96969 standard; cDNA; 893 BP.
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AC   ADM96969;
XX
DT   01-JUL-2004  (first entry)
XX
DE   Human pancreatic cancer upregulated gene C1958V2.
XX
KW   ds; gene; cytostatic; gene therapy; pancreatic cancer; diagnosis;
KW   anti-tumor immunity.
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OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
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XX
PN   WO2004031411-A2.
XX
PD   15-APR-2004.
XX
PF   12-SEP-2003; 2003WO-JP011713.
XX
PR   30-SEP-2002; 2002US-0414872P.
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PR 28-FEB-2003; 2003US-0450889P.
XX
PA (ONCO-) ONCOTHERAPY SCI INC.
PA (UYTY) UNIV TOKYO.
XX
PI Nakamura Y, Katagiri T;
XX
DR WPI; 2004-330204/30.
DR P-PSDB; ADM96970.
XX
PT New C1958V1 or C1958V2 polypeptides, useful in useful in diagnosing and
PT treating pancreatic cancer and in inducing anti tumor immunity.
XX
PS Claim 2; SEQ ID NO 3; 71pp; English.
XX
CC The invention relates to the isolation of novel genes upregulated in
CC pancreatic cancer designated C1958V1 and C1958V2, their encoded
CC polypeptides (I), a sequence in which one or more amino acids are
CC substituted, deleted, inserted, and/or added and that has a biological
CC activity equivalent to the C1958V1 or C1958V2 proteins; or a sequence
CC encoded by a polynucleotide that hybridizes under stringent conditions to
CC the C1958V1 or C1958V2 polynucleotides. The polypeptides and
CC polynucleotides, compounds and compositions are useful in diagnosing and
CC treating pancreatic cancer and in inducing anti tumor immunity. This
CC sequence represents the C1958V2 cDNA sequence.
XX
SQ Sequence 893 BP; 175 A; 287 C; 274 G; 157 T; 0 U; 0 Other;

Query Match 93.9%; Score 827; DB 2; Length 893;
Best Local Similarity 97.5%; Pred. No. 4.9e-193;
Matches 859; Conservative 0; Mismatches 0; Indels 22; Gaps 1;

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Qy          1 GGGCCATGACCCCCGCTGCTCTGTCTTGCAGGCTCGTCGCCGCGGCCCCCCGAGCCCGAC 60
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Qy        121 AGTGAGCCCACCAAGAAGGAAGCGGCCTGCAGAGGTGCCGACATGGGGCTTAAGATGTCC 180
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Qy        181 TGCCTGAAAGGCTTTCAAATGTGTGTCAGCAGCAGCAGCAGCCACGACGAGGCCCCC 240
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Qy         601 GACCGGACCTCTGACACCTCCAGGTTCTTGCTGACTCCGGCCTGGTGAAAGGGAGCGCCA 660
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         613 GACCGGACCTCTGACACCTCCAGGTTCTTGCTGACTCCGGCCTGGTGAAAGGGAGCGCCA 672

Qy         661 TGGTCCTGGCTGTTGGGGTCCCAGGGAGAGGCTCTCTTCTGGACAAACACACCCTCCCAG 720
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         673 TGGTCCTGGCTGTTGGGGTCCCAGGGAGAGGCTCTCTTCTGGACAAACACACCCTCCCAG 732

Qy         721 CCCCCAGGGCTGTGCAAACACATGCCCCTGCCATAAGCACCAACAAGAACTTCTTGCAGG 780
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         733 CCCCCAGGGCTGTGCAAACACATGCCCCTGCCATAAGCACCAACAAGAACTTCTTGCAGG 792

Qy         781 TGGAGTGGCTGTTTTTTATAAGTTGTTTTACAGATACGGAAACAGTCCAAAATGGGATTT 840
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         793 TGGAGTGGCTGTTTTTTATAAGTTGTTTTACAGATACGGAAACAGTCCAAAATGGGATTT 852

Qy         841 ATAATTTCTTTTTTGCATTATAAATAAAGATCCTCTGTAAC 881
                 |||||||||||||||||||||||||||||||||||||||||
Db         853 ATAATTTCTTTTTTGCATTATAAATAAAGATCCTCTGTAAC 893


RESULT 4
AES72473
ID   AES72473 standard; cDNA; 893 BP.
XX
AC   AES72473;
```

XX
DT 03-MAY-2007 (first entry)
XX
DE Human C1958 splice variant 3, cDNA.
XX
KW Pancreatic ductal adenocarcinoma; cancer; cytostatic; tumor marker;
KW protein therapy; screening; splice variant; ss; gene; C1958V3; apoptosis;
KW gene therapy; pancreas tumor; lung tumor; renal tumor; testicle tumor.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 197. .259
FT /*tag= a
FT /product= "C1958V3"
XX
PN WO2007013358-A2.
XX
PD 01-FEB-2007.
XX
PF 14-JUL-2006; 2006WO-JP314442.
XX
PR 28-JUL-2005; 2005US-0703791P.
XX
PA (ONCO-) ONCOTHERAPY SCI INC.
PA (UYTY) UNIV TOKYO.
XX
PI Nakamura Y, Katagiri T, Inaki K;
XX
DR WPI; 2007-283242/27.
DR P-PSDB; AES72474.
XX
PT New VIVIT polypeptide useful for treating or preventing cancer, such as
PT pancreatic cancer, lung cancer, kidney cancer and testicular tumor.
XX
PS Disclosure; SEQ ID NO 3; 78pp; English.
XX
CC The invention relates to a VIVIT polypeptide (AES72497) and at least a
CC fragment of the human C1958 sequence appearing as AES72472, in which
CC residues at positions 37-41 is replaced with AES72497, or an amino acid
CC sequence of a polypeptide functionally equivalent to the polypeptide
CC comprising the fragment sequence. Also included are an agent for
CC treating/preventing cancer (comprising as an active ingredient the VIVIT
CC polypeptide, or a polynucleotide encoding the polypeptide), a
CC pharmaceutical composition (comprising the VIVIT polypeptide, and a
CC carrier), screening (M1) for a compound useful in treating/preventing
CC cancers (involving (a) contacting a polypeptide comprising a PPP3CA-
CC binding domain of a C1958 polypeptide with a polypeptide comprising a
CC C1958-binding domain of a PPP3CA polypeptide in the presence of a test

CC compound, (b) detecting binding between the polypeptides, and (c)
CC selecting a test compound that inhibits binding between the
CC polypeptides), a kit for screening for a compound for treating or
CC preventing cancers, treating/preventing cancers in a subject (involving
CC administering the compound selected above), and inducing apoptosis in a
CC cell (involving introducing a polypeptide having a dominant-negative
CC effect against C1958 or a polynucleotide encoding the polypeptide into
CC the cell, where the polypeptide comprises a fragment sequence having
CC AES72497, or the mutated C1958 above). The polypeptide is modified with a
CC cell-membrane permeable substance, which has the general formula [R]-[D],
CC where [R] represents the cell-membrane permeable substance, and [D]
CC represents the amino acid sequence of a fragment sequence of AES72497, or
CC the mutated C1958 peptide. The VIVIT polypeptide is useful for treating
CC and/or preventing cancer, preferably pancreatic cancer (especially
CC Pancreatic ductal adenocarcinoma), lung cancer, kidney cancer and
CC testicular tumor. (M1) is useful for screening a compound for treating or
CC preventing cancers. The present sequence encodes a splice variant of
CC human C1958.
XX
SQ Sequence 893 BP; 175 A; 287 C; 274 G; 157 T; 0 U; 0 Other;

Query Match 93.9%; Score 827; DB 3; Length 893;
Best Local Similarity 97.5%; Pred. No. 4.9e-193;
Matches 859; Conservative 0; Mismatches 0; Indels 22; Gaps 1;

```
Qy          1 GGGCCATGACCCCCGCTGCTCTGTCTTGCAGGCTCGTCGCCGCGGCCCCCCGAGCCCGAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         35 GGGCCATGACCCCCGCTGCTCTGTCTTGCAGGCTCGTCGCCGCGGCCCCCCGAGCCCGAC 94

Qy         61 CGCCGCCGCCACCACCACCAGCGCCCGGGCGGGCCTCGCGCGCCTCGGGCGCGGCTCCGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         95 CGCCGCCGCCACCACCACCAGCGCCCGGGCGGGCCTCGCGCGCCTCGGGCGCGGCTCCGC 154

Qy        121 AGTGAGCCCACCAAGAAGGAAGCGGCCTGCAGAGGTGCCGACATGGGGCTTAAGATGTCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        155 AGTGAGCCCACCAAGAAGGAAGCGGCCTGCAGAGGTGCCGACATGGGGCTTAAGATGTCC 214

Qy        181 TGCCTGAAAGGCTTTCAAATGTGTGTCAGCAGCAGCAGCAGCAGCCACGACGAGGCCCCC 240
              ||||||||                              ||||||||||||||||||||||||||||||
Db        215 TGCCTGAA----------------------AGCAGCAGCAGCAGCCACGACGAGGCCCCC 252

Qy        241 GTCCTGAACGACAAGCACCTGGACGTGCCCGACATCATCATCACGCCCCCCACCCCCACG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        253 GTCCTGAACGACAAGCACCTGGACGTGCCCGACATCATCATCACGCCCCCCACCCCCACG 312

Qy        301 GGCATGATGCTGCCGAGGGACTTGGGGAGCACAGTCTGGCTGGATGAGACAGGGTCGTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        313 GGCATGATGCTGCCGAGGGACTTGGGGAGCACAGTCTGGCTGGATGAGACAGGGTCGTGC 372
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```
Qy        361 CCAGATGATGGAGAAATCGACCCAGAAGCCTGAGGAGGTGTCCTGGGTTTGGCTGGCTGG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        373 CCAGATGATGGAGAAATCGACCCAGAAGCCTGAGGAGGTGTCCTGGGTTTGGCTGGCTGG 432

Qy        421 CTCCTGCTCCAGCGGCCCGGCTTCAGGTGTCCGGGGGGCGTGGCTGCCTGGAGCAGGTGTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        433 CTCCTGCTCCAGCGGCCCGGCTTCAGGTGTCCGGGGGCGTGGCTGCCTGGAGCAGGTGTG 492

Qy        481 CTGAATACCCTGGATGGGAACTGAGCGAACCCGGGCCTCCGCTCAGAGAGACGTGGCAGG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        493 CTGAATACCCTGGATGGGAACTGAGCGAACCCGGGCCTCCGCTCAGAGAGACGTGGCAGG 552

Qy        541 ACCAGCGAGGAATCCAGCCTGTCCACTTCCAGAACAGTGTTTCCCAGGCCCCGCTGAGTG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        553 ACCAGCGAGGAATCCAGCCTGTCCACTTCCAGAACAGTGTTTCCCAGGCCCCGCTGAGTG 612

Qy        601 GACCGGACCTCTGACACCTCCAGGTTCTTGCTGACTCCGGCCTGGTGAAAGGGAGCGCCA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        613 GACCGGACCTCTGACACCTCCAGGTTCTTGCTGACTCCGGCCTGGTGAAAGGGAGCGCCA 672

Qy        661 TGGTCCTGGCTGTTGGGGTCCCAGGGAGAGGCTCTCTTCTGGACAAACACACCCTCCCAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        673 TGGTCCTGGCTGTTGGGGTCCCAGGGAGAGGCTCTCTTCTGGACAAACACACCCTCCCAG 732

Qy        721 CCCCCAGGGCTGTGCAAACACATGCCCCTGCCATAAGCACCAACAAGAACTTCTTGCAGG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        733 CCCCCAGGGCTGTGCAAACACATGCCCCTGCCATAAGCACCAACAAGAACTTCTTGCAGG 792

Qy        781 TGGAGTGGCTGTTTTTTATAAGTTGTTTTACAGATACGGAAACAGTCCAAAATGGGATTT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        793 TGGAGTGGCTGTTTTTTATAAGTTGTTTTACAGATACGGAAACAGTCCAAAATGGGATTT 852

Qy        841 ATAATTTCTTTTTTGCATTATAAATAAAGATCCTCTGTAAC 881
              |||||||||||||||||||||||||||||||||||||||||
Db        853 ATAATTTCTTTTTTGCATTATAAATAAAGATCCTCTGTAAC 893


RESULT 5
AAK88446
ID   AAK88446 standard; cDNA; 761 BP.
XX
AC   AAK88446;
XX
DT   05-NOV-2001  (first entry)
XX
DE   Human digestive system antigen coding sequence SEQ ID NO: 762.
XX
KW   Human; digestive system antigen; gene therapy; cancer; appendicitis;
KW   ulcerative colitis; infection; Hirschsprung's disease; chronic colitis;
```

```
KW   digestive system disorder; Meckel's diverticulum; ss.
XX
OS   Homo sapiens.
XX
PN   WO200155314-A2.
XX
PD   02-AUG-2001.
XX
PF   17-JAN-2001; 2001WO-US001324.
XX
PR   31-JAN-2000; 2000US-0179065P.
PR   04-FEB-2000; 2000US-0180628P.
PR   24-FEB-2000; 2000US-0184664P.
PR   02-MAR-2000; 2000US-0186350P.
PR   16-MAR-2000; 2000US-0189874P.
PR   17-MAR-2000; 2000US-0190076P.
PR   18-APR-2000; 2000US-0198123P.
PR   19-MAY-2000; 2000US-0205515P.
PR   07-JUN-2000; 2000US-0209467P.
PR   28-JUN-2000; 2000US-0214886P.
PR   30-JUN-2000; 2000US-0215135P.
PR   07-JUL-2000; 2000US-0216647P.
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PR   01-SEP-2000; 2000US-0229344P.
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PR 06-SEP-2000; 2000US-0230437P.
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PR 08-SEP-2000; 2000US-0231243P.
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PR 08-SEP-2000; 2000US-0231413P.
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PR 08-SEP-2000; 2000US-0232080P.
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PR 01-NOV-2000; 2000US-0244617P.

PR 08-NOV-2000; 2000US-0246474P.
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PR 08-NOV-2000; 2000US-0246610P.
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PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
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PR 17-NOV-2000; 2000US-0249210P.
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PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
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PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
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PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
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PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
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PR 05-DEC-2000; 2000US-0251030P.
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PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX

PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-502630/55.
DR P-PSDB; AAM92673.
XX
PT Polynucleotides encoding digestive system antigens, useful for
PT diagnosing, treating, preventing and/or prognozing disorders of the
PT digestive system, particularly cancer and cancer metastases.
XX
PS Claim 1; SEQ ID NO 762; 986pp; English.
XX
CC The present invention provides the protein and coding sequences of a
CC number of human digestive system antigens. These can be used in the
CC diagnosis, treatment and prevention of digestive system disorders,
CC including cancer, Meckel's diverticulum, bacterial or parasitic
CC infections, appendicitis, Hirschsprung's disease, chronic colitis or
CC ulcerative colitis. The present sequence is a cDNA encoding a digestive
CC system antigen of the invention
XX
SQ Sequence 761 BP; 183 A; 208 C; 218 G; 150 T; 0 U; 2 Other;

Query Match 79.8%; Score 703.2; DB 1; Length 761;
Best Local Similarity 99.3%; Pred. No. 1.4e-162;
Matches 735; Conservative 2; Mismatches 0; Indels 3; Gaps 3;

```
Qy        142 GCGGCCTGCAGAGGTGCCGACATGGGGCTTAAGATGTCCTGCCTGAAAGGCTTTCAAATG 201
              ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db          1 GCGGCCTGCAGAGGTGCCGACATGGGGCTTAAGATGTCCTGCCTGAAA-GCTTTCAAATG 59

Qy        202 TGTGTCAGCAGCAGCAGCAGCCACGACGAGGCCCCCGTCCTGAACGACAAGCACCTG 261
              |||||||||||||||||||||||||||||||| |||||||||||:|:|||||||||||
Db         60 TGTGTCAGCAGCAGCAGCAGCCACGACGAGG-CCCCGTCCTGAAMGWCAAGCACCTG 118

Qy        262 GACGTGCCCGACATCATCATCACGCCCCCCACCCCCACGGGCATGATGCTGCCGAGGGAC 321
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        119 GACGTGCCCGACATCATCATCACGCCCCCCA-CCCCACGGGCATGATGCTGCCGAGGGAC 177

Qy        322 TTGGGGAGCACAGTCTGGCTGGATGAGACAGGGTCGTGCCCAGATGATGGAGAAATCGAC 381
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        178 TTGGGGAGCACAGTCTGGCTGGATGAGACAGGGTCGTGCCCAGATGATGGAGAAATCGAC 237

Qy        382 CCAGAAGCCTGAGGAGGTGTCCTGGGTTTGGCTGGCTGGCTCCTGCTCCAGCGGCCCGGC 441
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 CCAGAAGCCTGAGGAGGTGTCCTGGGTTTGGCTGGCTGGCTCCTGCTCCAGCGGCCCGGC 297

Qy        442 TTCAGGTGTCCGGGGGCGTGGCTGCCTGGAGCAGGTGTGCTGAATACCCTGGATGGGAAC 501
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        298 TTCAGGTGTCCGGGGGCGTGGCTGCCTGGAGCAGGTGTGCTGAATACCCTGGATGGGAAC 357

Qy        502 TGAGCGAACCCGGGCCTCCGCTCAGAGAGACGTGGCAGGACCAGCGAGGAATCCAGCCTG 561
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        358 TGAGCGAACCCGGGCCTCCGCTCAGAGAGACGTGGCAGGACCAGCGAGGAATCCAGCCTG 417

Qy        562 TCCACTTCCAGAACAGTGTTTCCCAGGCCCCGCTGAGTGGACCGGACCTCTGACACCTCC 621
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        418 TCCACTTCCAGAACAGTGTTTCCCAGGCCCCGCTGAGTGGACCGGACCTCTGACACCTCC 477

Qy        622 AGGTTCTTGCTGACTCCGGCCTGGTGAAAGGGAGCGCCATGGTCCTGGCTGTTGGGGTCC 681
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        478 AGGTTCTTGCTGACTCCGGCCTGGTGAAAGGGAGCGCCATGGTCCTGGCTGTTGGGGTCC 537

Qy        682 CAGGGAGAGGCTCTCTTCTGGACAAACACACCCTCCCAGCCCCCAGGGCTGTGCAAACAC 741
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        538 CAGGGAGAGGCTCTCTTCTGGACAAACACACCCTCCCAGCCCCCAGGGCTGTGCAAACAC 597

Qy        742 ATGCCCCTGCCATAAGCACCAACAAGAACTTCTTGCAGGTGGAGTGGCTGTTTTTTATAA 801
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        598 ATGCCCCTGCCATAAGCACCAACAAGAACTTCTTGCAGGTGGAGTGGCTGTTTTTTATAA 657

Qy        802 GTTGTTTTACAGATACGGAAACAGTCCAAAATGGGATTTATAATTTCTTTTTTGCATTAT 861
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        658 GTTGTTTTACAGATACGGAAACAGTCCAAAATGGGATTTATAATTTCTTTTTTGCATTAT 717

Qy        862 AAATAAAGATCCTCTGTAAC 881
              ||||||||||||||||||||
Db        718 AAATAAAGATCCTCTGTAAC 737
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```
RESULT 6
AAI90742/c
ID   AAI90742 standard; cDNA; 963 BP.
XX
AC   AAI90742;
XX
DT   06-NOV-2001  (first entry)
XX
DE   Human polynucleotide SEQ ID NO 10802.
XX
KW   Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW   vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW   tissue growth factor; immunomodulatory; cancer; leukaemia;
KW   nervous system disorders; arthritis; inflammation; ss.
XX
OS   Homo sapiens.
XX
PN   WO200164835-A2.
```

XX
PD 07-SEP-2001.
XX
PF 26-FEB-2001; 2001WO-US004927.
XX
PR 28-FEB-2000; 2000US-00515126.
PR 18-MAY-2000; 2000US-00577409.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT;
XX
DR WPI; 2001-514838/56.
DR P-PSDB; AAO10811.
XX
PT Isolated nucleic acids and polypeptides, useful for preventing diagnosing
PT and treating e.g. leukemia, inflammation and immune disorders.
XX
PS Claim 1; SEQ ID NO 10802; 1399pp + Sequence Listing; English.
XX
CC The invention relates to human polynucleotides (AAI79941-AAI93841) and
CC the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 963 BP; 202 A; 296 C; 269 G; 194 T; 0 U; 2 Other;

Query Match 78.8%; Score 694.2; DB 1; Length 963;
Best Local Similarity 98.9%; Pred. No. 2.6e-160;
Matches 699; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 175 ATGTCCTGCCTGAAAGGCTTTCAAATGTGTGTCAGCAGCAGCAGCAGCAGCCACGACGAG 234
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Db 715 ACGCCTGGCTTCTCAGGCTTTCAAATGTGTGTCAGCAGCAGCAGCAGCAGCCACGACGAG 656

Qy 235 GCCCCCGTCCTGAACGACAAGCACCTGGACGTGCCCGACATCATCATCACGCCCCCCACC 294
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Qy 295 CCCACGGGCATGATGCTGCCGAGGGACTTGGGGAGCACAGTCTGGCTGGATGAGACAGGG 354

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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        595 CCCACGGGCATGATGCTGCCGAGGGACTTGGGGAGCACAGTCTGGCTGGATGAGACAGGG 536

Qy        355 TCGTGCCCAGATGATGGAGAAATCGACCCAGAAGCCTGAGGAGGTGTCCTGGGTTTGGCT 414
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        535 TCGTGCCCAGATGATGGAGAAATCGACCCAGAAGCCTGAGGAGGTGTCCTGGGTTTGGCT 476

Qy        415 GGCTGGCTCCTGCTCCAGCGGCCCGGCTTCAGGTGTCCGGGGGGCGTGGCTGCCTGGAGCA 474
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        475 GGCTGGCTCCTGCTCCAGCGGCCCGGCTTCAGGTGTCCGGGGGGCGTGGCTGCCTGGAGCA 416

Qy        475 GGTGTGCTGAATACCCTGGATGGGAACTGAGCGAACCCGGGCCTCCGCTCAGAGAGACGT 534
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        415 GGTGTGCTGAATACCCTGGATGGGAACTGAGCGAACCCGGGCCTCCGCTCAGAGAGACGT 356

Qy        535 GGCAGGACCAGCGAGGAATCCAGCCTGTCCACTTCCAGAACAGTGTTTCCCAGGCCCCGC 594
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        355 GGCAGGACCAGCGAGGAATCCAGCCTGTCCACTTCCAGAACAGTGTTTCCCAGGCCCCGC 296

Qy        595 TGAGTGGACCGGACCTCTGACACCTCCAGGTTCTTGCTGACTCCGGCCTGGTGAAAGGGA 654
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        295 TGAGTGGACCGGACCTCTGACACCTCCAGGTTCTTGCTGACTCCGGCCTGGTGAAAGGGA 236

Qy        655 GCGCCATGGTCCTGGCTGTTGGGGTCCCAGGGAGAGGCTCTCTTCTGGACAAACACACCC 714
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        235 GCGCCATGGTCCTGGCTGTTGGGGTCCCAGGGAGAGGCTCTCTTCTGGACAAACACACCC 176

Qy        715 TCCCAGCCCCCAGGGCTGTGCAAACACATGCCCCTGCCATAAGCACCAACAAGAACTTCT 774
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        175 TCCCAGCCCCCAGGGCTGTGCAAACACATGCCCCTGCCATAAGCACCAACAAGAACTTCT 116

Qy        775 TGCAGGTGGAGTGGCTGTTTTTTATAAGTTGTTTTACAGATACGGAAACAGTCCAAAATG 834
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        115 TGCAGGTGGAGTGGCTGTTTTTTATAAGTTGTTTTACAGATACGGAAACAGTCCAAAATG 56

Qy        835 GGATTTATAATTTCTTTTTTGCATTATAAATAAAGATCCTCTGTAAC 881
                |||||||||||||||||||||||||||||||||||||||||||||
Db         55 GGATTTATAATTTCTTTTTTGCATTATAAATAAAGATCCTCTGTAAC 9
```

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RESULT 7
ADE09694/c
ID   ADE09694 standard; DNA; 963 BP.
XX
AC   ADE09694;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Novel DNA-related contig nucleotide sequence #416.
```

```
XX
KW   novel gene; novel protein; tissue marker; molecular weight marker;
KW   chromosome marker; genetic disorder; contig; ds.
XX
OS   Unidentified.
XX
PN   WO2003054152-A2.
XX
PD   03-JUL-2003.
XX
PF   10-DEC-2002; 2002WO-US039555.
XX
PR   10-DEC-2001; 2001US-0339739P.
PR   11-DEC-2001; 2001US-0339453P.
PR   14-MAR-2002; 2002US-0365091P.
PR   14-MAR-2002; 2002US-0365384P.
PR   12-APR-2002; 2002US-0372381P.
PR   12-APR-2002; 2002US-0372615P.
PR   22-APR-2002; 2002US-00128558.
PR   24-APR-2002; 2002US-0376045P.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT,  Asundi V,  Goodrich RW,  Ren F,  Zhang J,  Zhao QA,  Wang J;
PI   Ghosh M,  Xue AJ,  Wehrman T,  Weng G,  Zhou P,  Drmanac RT,  Wang Z;
PI   Ma Y,  Wang D,  Chen R,  Xu C,  Boyle BJ;
XX
DR   WPI; 2003-569235/53.
XX
PT   New polynucleotides, useful for expressing recombinant proteins for
PT   analysis, characterization or therapeutic use, or as markers for tissues
PT   in which the corresponding protein is preferentially expressed.
XX
PS   Disclosure; SEQ ID NO 2238; 1177pp; English.
XX
CC   The invention comprises the amino acid and coding sequences of novel
CC   proteins. The DNA and protein sequences of the invention are useful as:
CC   markers for tissues in which the corresponding protein is preferentially
CC   expressed; as molecular weight markers on gels; as chromosome markers or
CC   tags; to identify chromosomes or to map related gene positions; and to
CC   compare with endogenous DNA sequences in patients to identify potential
CC   genetic disorders. The present DNA sequence was used in the
CC   exemplification of the invention.
XX
SQ   Sequence 963 BP; 202 A; 296 C; 269 G; 194 T; 0 U; 2 Other;

  Query Match             78.8%;  Score 694.2;  DB 1;  Length 963;
  Best Local Similarity   98.9%;  Pred. No. 2.6e-160;
  Matches  699;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;
```

```
Qy        175 ATGTCCTGCCTGAAAGGCTTTCAAATGTGTGTCAGCAGCAGCAGCAGCAGCCCACGACGAG 234
              | | |   || |   ||||||||||||||||||||||||||||||||||||||||||||||||
Db        715 ACGCCTGGCTTCTCAGGCTTTCAAATGTGTGTCAGCAGCAGCAGCAGCAGCCACGACGAG 656

Qy        235 GCCCCCGTCCTGAACGACAAGCACCTGGACGTGCCCGACATCATCATCACGCCCCCCACC 294
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        655 GCCCCCGTCCTGAACGACAAGCACCTGGACGTGCCCGACATCATCATCACGCCCCCCACC 596

Qy        295 CCCACGGGCATGATGCTGCCGAGGGACTTGGGGAGCACAGTCTGGCTGGATGAGACAGGG 354
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        595 CCCACGGGCATGATGCTGCCGAGGGACTTGGGGAGCACAGTCTGGCTGGATGAGACAGGG 536

Qy        355 TCGTGCCCAGATGATGGAGAAATCGACCCAGAAGCCTGAGGAGGTGTCCTGGGTTTGGCT 414
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        535 TCGTGCCCAGATGATGGAGAAATCGACCCAGAAGCCTGAGGAGGTGTCCTGGGTTTGGCT 476

Qy        415 GGCTGGCTCCTGCTCCAGCGGCCCGGCTTCAGGTGTCCGGGGGGCGTGGCTGCCTGGAGCA 474
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        475 GGCTGGCTCCTGCTCCAGCGGCCCGGCTTCAGGTGTCCGGGGGGCGTGGCTGCCTGGAGCA 416

Qy        475 GGTGTGCTGAATACCCTGGATGGGAACTGAGCGAACCCGGGCCTCCGCTCAGAGAGACGT 534
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        415 GGTGTGCTGAATACCCTGGATGGGAACTGAGCGAACCCGGGCCTCCGCTCAGAGAGACGT 356

Qy        535 GGCAGGACCAGCGAGGAATCCAGCCTGTCCACTTCCAGAACAGTGTTTCCCAGGCCCCGC 594
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        355 GGCAGGACCAGCGAGGAATCCAGCCTGTCCACTTCCAGAACAGTGTTTCCCAGGCCCCGC 296

Qy        595 TGAGTGGACCGGACCTCTGACACCTCCAGGTTCTTGCTGACTCCGGCCTGGTGAAAGGGA 654
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        295 TGAGTGGACCGGACCTCTGACACCTCCAGGTTCTTGCTGACTCCGGCCTGGTGAAAGGGA 236

Qy        655 GCGCCATGGTCCTGGCTGTTGGGGTCCCAGGGAGAGGCTCTCTTCTGGACAAACACACCC 714
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        235 GCGCCATGGTCCTGGCTGTTGGGGTCCCAGGGAGAGGCTCTCTTCTGGACAAACACACCC 176

Qy        715 TCCCAGCCCCCAGGGCTGTGCAAACACATGCCCCTGCCATAAGCACCAACAAGAACTTCT 774
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        175 TCCCAGCCCCCAGGGCTGTGCAAACACATGCCCCTGCCATAAGCACCAACAAGAACTTCT 116

Qy        775 TGCAGGTGGAGTGGCTGTTTTTTATAAGTTGTTTTACAGATACGGAAACAGTCCAAAATG 834
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        115 TGCAGGTGGAGTGGCTGTTTTTTATAAGTTGTTTTACAGATACGGAAACAGTCCAAAATG 56

Qy        835 GGATTTATAATTTCTTTTTTGCATTATAAATAAAGATCCTCTGTAAC 881
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db         55 GGATTTATAATTTCTTTTTTGCATTATAAATAAAGATCCTCTGTAAC 9
```

RESULT 8
ARC01157
ID ARC01157 standard; DNA; 1239 BP.
XX
AC ARC01157;
XX
DT 10-JUL-2008 (first entry)
XX
DE DNA fragments of a human Tox gene, 45208.
XX
KW DNA microarray; gene expression; drug screening; ds; Tox.
XX
OS Homo sapiens.
XX
PN US2007072175-A1.
XX
PD 29-MAR-2007.
XX
PF 15-MAY-2006; 2006US-00433832.
XX
PR 13-MAY-2005; 2005US-0680473P.
PR 13-MAY-2005; 2005US-0680544P.
XX
PA (BIOJ) BIOGEN IDEC MA INC.
XX
PI Cooper MT, Kinch D, Rosenberg M, Subramaniam SS, Szak ST, Li H;
PI Bandaru R, Derbel M;
XX
DR WPI; 2007-432796/41.
XX
PT New nucleotide array comprises polynucleotide probes complementary to, or
PT fragments of, Cynomolgus monkey genes, useful for detecting changes in
PT gene expression upon administration of a therapeutic agent.
XX
PS Claim 18; SEQ ID NO 45208; 33pp; English.
XX
CC The new invention relates to a nucleotide array for detecting changes in
CC gene expression upon administration of a therapeutic agent. The
CC microarray has polynucleotide probes complementary to, or fragments of,
CC Cynomolgus monkey genes, where each polynucleotide probe is immobilized
CC to a discrete and known spot on a solid support. The polynucleotide
CC probes are complementary to, or fragments of, any portion of an ortholog
CC of a human gene, preferably a Tox gene. The probes are any of SEQ ID NO.
CC 8882-9186. The probes are also complementary to, or fragments of, any
CC portion of any of SEQ ID NO. 1-8881 or 9187-18598. The nucleotide array
CC has at least one probe complementary to, or a fragment of, any portion of
CC any human gene, where the probe from a human gene is any of SEQ ID NO.
CC 43226-48714, or is complementary to, or a fragment of, any portion of any

CC of SEQ ID NO. 43450-48714. The array has at least one probe complementary
CC to, or a fragment of, any portion of any Rhesus monkey gene, where the
CC probe from a Rhesus monkey gene is any of SEQ ID NO. 35841-36074, or is
CC complementary to, or a fragment of, any portion of any of SEQ ID NO.
CC 18599-35840 or 36075-43225. It also has at least one probe complementary
CC to, or a fragment of, any portion of a Rhesus monkey gene and at least
CC one probe complementary to, or a fragment of, any portion of any human
CC gene. The nucleotide array is useful for detecting changes in gene
CC expression upon administration of a therapeutic agent. It can be used for
CC characterizing the actions, targets, and toxicities of therapeutic agents
CC in primates, e.g. a human, a Cynomolgus monkey, or a Rhesus monkey. This
CC sequence is a DNA fragment of a human Tox gene.
XX
SQ Sequence 1239 BP; 262 A; 331 C; 391 G; 255 T; 0 U; 0 Other;

Query Match 78.8%; Score 694.2; DB 3; Length 1239;
Best Local Similarity 98.9%; Pred. No. 2.8e-160;
Matches 699; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

```
Qy        175 ATGTCCTGCCTGAAAGGCTTTCAAATGTGTGTCAGCAGCAGCAGCAGCAGCCACGACGAG 234
              | | |  || |   ||||||||||||||||||||||||||||||||||||||||||||||
Db        528 ACGCCTGGCTTCTCAGGCTTTCAAATGTGTGTCAGCAGCAGCAGCAGCCACGACGAG 587

Qy        235 GCCCCCGTCCTGAACGACAAGCACCTGGACGTGCCCGACATCATCATCACGCCCCCCACC 294
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        588 GCCCCCGTCCTGAACGACAAGCACCTGGACGTGCCCGACATCATCATCACGCCCCCCACC 647

Qy        295 CCCACGGGCATGATGCTGCCGAGGGACTTGGGGAGCACAGTCTGGCTGGATGAGACAGGG 354
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        648 CCCACGGGCATGATGCTGCCGAGGGACTTGGGGAGCACAGTCTGGCTGGATGAGACAGGG 707

Qy        355 TCGTGCCCAGATGATGGAGAAATCGACCCAGAAGCCTGAGGAGGTGTCCTGGGTTTGGCT 414
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        708 TCGTGCCCAGATGATGGAGAAATCGACCCAGAAGCCTGAGGAGGTGTCCTGGGTTTGGCT 767

Qy        415 GGCTGGCTCCTGCTCCAGCGGCCCGGCTTCAGGTGTCCGGGGGGCGTGGCTGCCTGGAGCA 474
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        768 GGCTGGCTCCTGCTCCAGCGGCCCGGCTTCAGGTGTCCGGGGGGCGTGGCTGCCTGGAGCA 827

Qy        475 GGTGTGCTGAATACCCTGGATGGGAACTGAGCGAACCCGGGCCTCCGCTCAGAGAGACGT 534
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        828 GGTGTGCTGAATACCCTGGATGGGAACTGAGCGAACCCGGGCCTCCGCTCAGAGAGACGT 887

Qy        535 GGCAGGACCAGCGAGGAATCCAGCCTGTCCACTTCCAGAACAGTGTTTCCCAGGCCCCGC 594
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        888 GGCAGGACCAGCGAGGAATCCAGCCTGTCCACTTCCAGAACAGTGTTTCCCAGGCCCCGC 947

Qy        595 TGAGTGGACCGGACCTCTGACACCTCCAGGTTCTTGCTGACTCCGGCCTGGTGAAAGGGA 654
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        948 TGAGTGGACCGGACCTCTGACACCTCCAGGTTCTTGCTGACTCCGGCCTGGTGAAAGGGA 1007

Qy        655 GCGCCATGGTCCTGGCTGTTGGGGTCCCAGGGAGAGGCTCTCTTCTGGACAAACACACCC 714
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1008 GCGCCATGGTCCTGGCTGTTGGGGTCCCAGGGAGAGGCTCTCTTCTGGACAAACACACCC 1067

Qy        715 TCCCAGCCCCCAGGGCTGTGCAAACACATGCCCCTGCCATAAGCACCAACAAGAACTTCT 774
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1068 TCCCAGCCCCCAGGGCTGTGCAAACACATGCCCCTGCCATAAGCACCAACAAGAACTTCT 1127

Qy        775 TGCAGGTGGAGTGGCTGTTTTTTATAAGTTGTTTTACAGATACGGAAACAGTCCAAAATG 834
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1128 TGCAGGTGGAGTGGCTGTTTTTTATAAGTTGTTTTACAGATACGGAAACAGTCCAAAATG 1187

Qy        835 GGATTTATAATTTCTTTTTTGCATTATAAATAAAGATCCTCTGTAAC 881
              |||||||||||||||||||||||||||||||||||||||||||||||
Db       1188 GGATTTATAATTTCTTTTTTGCATTATAAATAAAGATCCTCTGTAAC 1234


RESULT 9
AQD66153
ID   AQD66153 standard; DNA; 1261 BP.
XX
AC   AQD66153;
XX
DT   20-MAR-2008  (first entry)
XX
DE   Human chromosome 16 ORF 74 DNA SEQ ID 42.
XX
KW   diagnostic; therapeutic; prophylaxis; gene expression; tumor suppressor;
KW   dna library; peptide library; hybridoma; antibody production;
KW   antibody identification; gene transfer; vector; immunoassay; cancer;
KW   ovary tumor; cytostatic; chromosome-16; ORF 74; gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO2007147265-A1.
XX
PD   27-DEC-2007.
XX
PF   22-JUN-2007; 2007WO-CA001134.
XX
PR   23-JUN-2006; 2006US-0815829P.
PR   13-DEC-2006; 2006US-0874471P.
XX
PA   (ALET-) ALETHIA BIOTHERAPEUTIQUES INC.
XX
PI   Sooknanan RR,  Tremblay GB,  Filion M;
XX
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DR WPI; 2008-B28167/08.
DR P-PSDB; AQD66196.
DR PC:NCBI; gi14290598.
DR PC_ENCPRO:NCBI; gi14290599.
XX
PT new isolated polynucleotides and polypeptides involved in cancer, useful
PT for diagnosing, treating, or preventing cancer, e.g. ovarian cancer,
PT prostate cancer, breast cancer, lung cancer, or colon cancer.
XX
PS Claim 1; SEQ ID NO 42; 309pp; English.
XX
CC The present invention relates to novel isolated polynucleotides and
CC polypeptides involved in cancer, useful for diagnosing, treating, or
CC preventing cancer, particularly ovarian cancer. The invention further
CC relates to a vector comprising the polynucleotide; a library of
CC polynucleotide or polypeptide; a pharmaceutical composition comprising
CC the polynucleotide or polypeptide; use of the polynucleotide or
CC polypeptide in the manufacture of a composition for identification or
CC detection of a cancer cell; a method of reducing or slowing the growth of
CC a cancer cell in an individual; a siRNA or shRNA molecule that lowers the
CC expression of the polynucleotide; a kit for the diagnosis of cancer
CC comprising at least one polynucleotide or polypeptide or a reagent
CC capable of specifically binding to at least one polynucleotide or
CC polypeptide of the invention; an isolated or purified antibody and
CC antigen-binding fragment capable of specifically binding to the
CC polypeptide; a hybridoma cell producing an antibody capable of
CC specifically binding to a polypeptide of the invention; a composition
CC comprising the antibody; a method of making an antibody; a method of
CC identifying a compound that inhibits the activity or function of a
CC polypeptide of the invention; a cell transformed with the polynucleotide
CC or vector, or comprising an exogenous form of the polypeptide; a method
CC of identifying a compound that inhibits the expression of a
CC polynucleotide of the invention; and an immunoassay for detection of
CC antibodies that specifically bind to any one polypeptide of the
CC invention. The polynucleotide or polypeptide is useful in the
CC identification or detection of a cancer cell or in the manufacture of a
CC composition for identification or detection of a cancer cell or for
CC inhibiting the growth of an ovarian cancer cell. The polypeptide is
CC useful for detecting an antibody, which specifically binds to the
CC polypeptide which acts as a inhibitor of the polypeptide and is useful in
CC the treatment of cancer. The present sequence encodes a polypeptide
CC sequence of the invention which is used for the treatment of cancer.
CC
CC Revised record issued on 04-MAR-2008 : Enhanced with precomputed
CC information from BOND.
XX
SQ Sequence 1261 BP; 286 A; 332 C; 389 G; 254 T; 0 U; 0 Other;

Query Match 78.6%; Score 692.6; DB 4; Length 1261;

Best Local Similarity 98.7%; Pred. No. 7e-160;
Matches 698; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

```
Qy        175 ATGTCCTGCCTGAAAGGCTTTCAAATGTGTGTCAGCAGCAGCAGCAGCAGCCACGACGAG 234
              | | |  || |   ||||||||||||||||||||||||||||||||||||||||||||
Db        528 ACGCCTGGCTTCTCAGGCTTTCAAATGTGTGTCAGCAGCAGCAGCAGCAGCCACGACGAG 587

Qy        235 GCCCCCGTCCTGAACGACAAGCACCTGGACGTGCCCGACATCATCATCACGCCCCCCACC 294
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        588 GCCCCCGTCCTGAACGACAAGCACCTGGACGTGCCCGACATCATCATCACGCCCCCCACC 647

Qy        295 CCCACGGGCATGATGCTGCCGAGGGACTTGGGGAGCACAGTCTGGCTGGATGAGACAGGG 354
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        648 CCCACGGGCATGATGCTGCCGAGGGACTTGGGGAGCACAGTCTGGCTGGATGAGACAGGG 707

Qy        355 TCGTGCCCAGATGATGGAGAAATCGACCCAGAAGCCTGAGGAGGTGTCCTGGGTTTGGCT 414
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        708 TCGTGCCCAGATGATGGAGAAATCGACCCAGAAGCCTGAGGAGGTGTCCTGGGTTTGGCT 767

Qy        415 GGCTGGCTCCTGCTCCAGCGGCCCGGCTTCAGGTGTCCGGGGGGCGTGGCTGCCTGGAGCA 474
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        768 GGCTGGCTCCTGCTCCAGCGGCCCGGCTTCAGGTGTCCGGGGGGCGTGGCTGCCTGGAGCA 827

Qy        475 GGTGTGCTGAATACCCTGGATGGGAACTGAGCGAACCCGGGCCTCCGCTCAGAGAGACGT 534
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        828 GGTGTGCTGAATACCCTGGATGGGAACTGAGCGAACCCGGGCCTCCGCTCAGAGAGACGT 887

Qy        535 GGCAGGACCAGCGAGGAATCCAGCCTGTCCACTTCCAGAACAGTGTTTCCCAGGCCCCGC 594
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        888 GGCAGGACCAGCGAGGAATCCAGCCTGTCCACTTCCAGAACAGTGTTTCCCAGGCCCCGC 947

Qy        595 TGAGTGGACCGGACCTCTGACACCTCCAGGTTCTTGCTGACTCCGGCCTGGTGAAAGGGA 654
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        948 TGAGTGGACCGGACCTCTGACACCTCCAGGTTCTTGCTGACTCCGGCCTGGTGAAAGGGA 1007

Qy        655 GCGCCATGGTCCTGGCTGTTGGGGTCCCAGGGAGAGGCTCTCTTCTGGACAAACACACCC 714
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1008 GCGCCATGGTCCTGGCTGTTGGGGTCCCAGGGAGAGGCTCTCTTCTGGACAAACACACCC 1067

Qy        715 TCCCAGCCCCCAGGGCTGTGCAAACACATGCCCCTGCCATAAGCACCAACAAGAACTTCT 774
              |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db       1068 TCCCAGCCCCCAGGGCTGTGCAAACACATGCCCCTCCCATAAGCACCAACAAGAACTTCT 1127

Qy        775 TGCAGGTGGAGTGGCTGTTTTTTATAAGTTGTTTTACAGATACGGAAACAGTCCAAAATG 834
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1128 TGCAGGTGGAGTGGCTGTTTTTTATAAGTTGTTTTACAGATACGGAAACAGTCCAAAATG 1187

Qy        835 GGATTTATAATTTCTTTTTTGCATTATAAATAAAGATCCTCTGTAAC 881
              |||||||||||||||||||||||||||||||||||||||||||||||
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Db 1188 GGATTTATAATTTCTTTTTTGCATTATAAATAAAGATCCTCTGTAAC 1234

RESULT 10
ADR26670/c
ID ADR26670 standard; DNA; 614 BP.
XX
AC ADR26670;
XX
DT 21-OCT-2004 (first entry)
XX
DE Breast cancer prognosis marker #2531.
XX
KW ds; breast cancer; prognosis; gene expression; diagnosis.
XX
OS Homo sapiens.
XX
PN WO2004065545-A2.
XX
PD 05-AUG-2004.
XX
PF 15-JAN-2004; 2004WO-US001100.
XX
PR 15-JAN-2003; 2003US-00342887.
XX
PA (ROSE-) ROSETTA INPHARMATICS LLC.
PA (NECA-) NETHERLANDS CANCER INST.
XX
PI Van't Veer LJ, He Y;
XX
DR WPI; 2004-593473/57.
XX
PT Classifying a breast cancer patient according to prognosis comprises
PT determining the similarity between the level of expression of each of
PT five genes in a cell sample taken from patient, to control levels.
XX
PS Disclosure; SEQ ID NO 2531; 226pp; English.
XX
CC The invention relates to a method of classifying a breast cancer patient
CC according to prognosis by determining the similarity between the level of
CC expression of each of five genes for which markers are listed in the
CC specification, in a cell sample taken from the breast cancer patient, to
CC control levels of expression for each respective five genes to obtain a
CC patient similarity value. The methods are useful for classifying a breast
CC cancer patient according to prognosis. Kits and computer program products
CC are useful for data analysis using the diagnostic, prognostic and
CC statistical methods of the invention. This sequence corresponds to a
CC marker used in the method of the invention.
XX

```
SQ   Sequence 614 BP; 130 A; 179 C; 171 G; 134 T; 0 U; 0 Other;

  Query Match             69.4%;  Score 611;  DB 2;  Length 614;
  Best Local Similarity   100.0%;  Pred. No. 6.8e-140;
  Matches  611;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        271 GACATCATCATCACGCCCCCCACCCCCACGGGCATGATGCTGCCGAGGGACTTGGGGAGC 330
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        614 GACATCATCATCACGCCCCCCACCCCCACGGGCATGATGCTGCCGAGGGACTTGGGGAGC 555

Qy        331 ACAGTCTGGCTGGATGAGACAGGGTCGTGCCCAGATGATGGAGAAATCGACCCAGAAGCC 390
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        391 TGAGGAGGTGTCCTGGGTTTGGCTGGCTGGCTCCTGCTCCAGCGGCCCGGCTTCAGGTGT 450
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Qy        451 CCGGGGGCGTGGCTGCCTGGAGCAGGTGTGCTGAATACCCTGGATGGGAACTGAGCGAAC 510
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Db        434 CCGGGGGCGTGGCTGCCTGGAGCAGGTGTGCTGAATACCCTGGATGGGAACTGAGCGAAC 375

Qy        511 CCGGGCCTCCGCTCAGAGAGACGTGGCAGGACCAGCGAGGAATCCAGCCTGTCCACTTCC 570
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Db        374 CCGGGCCTCCGCTCAGAGAGACGTGGCAGGACCAGCGAGGAATCCAGCCTGTCCACTTCC 315

Qy        571 AGAACAGTGTTTCCCAGGCCCCGCTGAGTGGACCGGACCTCTGACACCTCCAGGTTCTTG 630
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Qy        631 CTGACTCCGGCCTGGTGAAAGGGAGCGCCATGGTCCTGGCTGTTGGGGTCCCAGGGAGAG 690
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Qy        691 GCTCTCTTCTGGACAAACACACCCTCCCAGCCCCCAGGGCTGTGCAAACACATGCCCCTG 750
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Qy        751 CCATAAGCACCAACAAGAACTTCTTGCAGGTGGAGTGGCTGTTTTTTATAAGTTGTTTTA 810
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Db        134 CCATAAGCACCAACAAGAACTTCTTGCAGGTGGAGTGGCTGTTTTTTATAAGTTGTTTTA  75

Qy        811 CAGATACGGAAACAGTCCAAAATGGGATTTATAATTTCTTTTTTGCATTATAAATAAAGA 870
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Db         74 CAGATACGGAAACAGTCCAAAATGGGATTTATAATTTCTTTTTTGCATTATAAATAAAGA  15

Qy        871 TCCTCTGTAAC 881
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RESULT 11
AAK90422
ID AAK90422 standard; DNA; 2798 BP.
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AC AAK90422;
XX
DT 05-NOV-2001 (first entry)
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DE Human digestive system antigen genomic sequence SEQ ID NO: 3998.
XX
KW Human; digestive system antigen; gene therapy; cancer; appendicitis;
KW ulcerative colitis; infection; Hirschsprung's disease; chronic colitis;
KW digestive system disorder; Meckel's diverticulum; ds.
XX
OS Homo sapiens.
XX
PN WO200155314-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US001324.
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XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-502630/55.
XX
PT Polynucleotides encoding digestive system antigens, useful for
PT diagnosing, treating, preventing and/or prognozing disorders of the
PT digestive system, particularly cancer and cancer metastases.
XX
PS Disclosure; SEQ ID NO 3998; 986pp; English.
XX
CC The present invention provides the protein and coding sequences of a
CC number of human digestive system antigens. These can be used in the
CC diagnosis, treatment and prevention of digestive system disorders,
CC including cancer, Meckel's diverticulum, bacterial or parasitic
CC infections, appendicitis, Hirschsprung's disease, chronic colitis or
CC ulcerative colitis. The present sequence is a genomic DNA fragment
CC encoding a digestive system antigen of the invention
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SQ Sequence 2798 BP; 594 A; 775 C; 809 G; 620 T; 0 U; 0 Other;

Query Match 62.3%; Score 549; DB 1; Length 2798;
Best Local Similarity 100.0%; Pred. No. 2.2e-124;
Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 393 AGGAGGTGTCCTGGGTTTGGCTGGCTGGCTCCTGCTCCAGCGGCCCGGCTTCAGGTGTCC 452
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Db 2300 AGGAGGTGTCCTGGGTTTGGCTGGCTGGCTCCTGCTCCAGCGGCCCGGCTTCAGGTGTCC 2359

Qy 453 GGGGGCGTGGCTGCCTGGAGCAGGTGTGCTGAATACCCTGGATGGGAACTGAGCGAACCC 512

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Qy        513 GGGCCTCCGCTCAGAGAGACGTGGCAGGACCAGCGAGGAATCCAGCCTGTCCACTTCCAG 572
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Db       2480 AACAGTGTTTCCCAGGCCCCGCTGAGTGGACCGGACCTCTGACACCTCCAGGTTCTTGCT 2539

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Qy        693 TCTCTTCTGGACAAACACACCCTCCCAGCCCCCAGGGCTGTGCAAACACATGCCCCTGCC 752
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Db       2720 GATACGGAAACAGTCCAAAATGGGATTTATAATTTCTTTTTTGCATTATAAATAAAGATC 2779

Qy        873 CTCTGTAAC 881
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Db       2780 CTCTGTAAC 2788


RESULT 12
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ID   AAK90423 standard; DNA; 2804 BP.
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AC   AAK90423;
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DT   05-NOV-2001  (first entry)
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DE   Human digestive system antigen genomic sequence SEQ ID NO: 3999.
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KW   Human; digestive system antigen; gene therapy; cancer; appendicitis;
KW   ulcerative colitis; infection; Hirschsprung's disease; chronic colitis;
KW   digestive system disorder; Meckel's diverticulum; ds.
XX
OS   Homo sapiens.
XX
PN   WO200155314-A2.
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PD 02-AUG-2001.
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PF 17-JAN-2001; 2001WO-US001324.
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XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-502630/55.

XX
PT Polynucleotides encoding digestive system antigens, useful for
PT diagnosing, treating, preventing and/or prognozing disorders of the
PT digestive system, particularly cancer and cancer metastases.
XX
PS Disclosure; SEQ ID NO 3999; 986pp; English.
XX
CC The present invention provides the protein and coding sequences of a
CC number of human digestive system antigens. These can be used in the
CC diagnosis, treatment and prevention of digestive system disorders,
CC including cancer, Meckel's diverticulum, bacterial or parasitic
CC infections, appendicitis, Hirschsprung's disease, chronic colitis or
CC ulcerative colitis. The present sequence is a genomic DNA fragment
CC encoding a digestive system antigen of the invention
XX
SQ Sequence 2804 BP; 598 A; 777 C; 808 G; 621 T; 0 U; 0 Other;

Query Match 62.1%; Score 547.4; DB 1; Length 2804;
Best Local Similarity 99.8%; Pred. No. 5.3e-124;
Matches 548; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy        393 AGGAGGTGTCCTGGGTTTGGCTGGCTGGCTCCTGCTCCAGCGGCCCGGCTTCAGGTGTCC 452
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Db       2306 AGGAGGTGTCCTGGGTTTGGCTGGCTGGCTCCTGCTCCAGCGGCCCGGCTTCAGGTGTCC 2365

Qy        453 GGGGGCGTGGCTGCCTGGAGCAGGTGTGCTGAATACCCTGGATGGGAACTGAGCGAACCC 512
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2366 GGGGGCGTGGCTGCCTGGAGCAGGTGTGCTGAATACCCTGGATGGGAACTGAGCGAACCC 2425

Qy        513 GGGCCTCCGCTCAGAGAGACGTGGCAGGACCAGCGAGGAATCCAGCCTGTCCACTTCCAG 572
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2426 GGGCCTCCGCTCAGAGAGACGTGGCAGGACCAGCGAGGAATCCAGCCTGTCCACTTCCAG 2485

Qy        573 AACAGTGTTTCCCAGGCCCCGCTGAGTGGACCGGACCTCTGACACCTCCAGGTTCTTGCT 632
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2486 AACAGTGTTTCCCAGGCCCCGCTGAGTGGACCGGACCTCTGACACCTCCAGGTTCTTGCT 2545

Qy        633 GACTCCGGCCTGGTGAAAGGGAGCGCCATGGTCCTGGCTGTTGGGGTCCCAGGGAGAGGC 692
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2546 GACTCCGGCCTGGTGAAAGGGAGCGCCATGGTCCTGGCTGTTGGGGTCCCAGGGAGAGGC 2605

Qy        693 TCTCTTCTGGACAAACACACCCTCCCAGCCCCCAGGGCTGTGCAAACACATGCCCCTGCC 752
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db       2606 TCTCTTCTGGACAAACACACCCTCCCAGCCCCCAGGGCTGTGCAAACACATGCCCCTCCC 2665
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Qy        753 ATAAGCACCAACAAGAACTTCTTGCAGGTGGAGTGGCTGTTTTTTATAAGTTGTTTTACA 812
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2666 ATAAGCACCAACAAGAACTTCTTGCAGGTGGAGTGGCTGTTTTTTATAAGTTGTTTTACA 2725

Qy        813 GATACGGAAACAGTCCAAAATGGGATTTATAATTTCTTTTTTGCATTATAAATAAAGATC 872
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2726 GATACGGAAACAGTCCAAAATGGGATTTATAATTTCTTTTTTGCATTATAAATAAAGATC 2785

Qy        873 CTCTGTAAC 881
              |||||||||
Db       2786 CTCTGTAAC 2794


RESULT 13
ABL65256
ID   ABL65256 standard; DNA; 574 BP.
XX
AC   ABL65256;
XX
DT   11-JUN-2007  (revised)
DT   15-MAY-2002  (first entry)
XX
DE   Lung cancer related gene sequence SEQ ID NO:3593.
XX
KW   Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW   stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW   cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
KW   gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO200194629-A2.
XX
PD   13-DEC-2001.
XX
PF   30-MAY-2001; 2001WO-US010838.
XX
PR   05-JUN-2000; 2000US-0209473P.
PR   05-JUN-2000; 2000US-0209531P.
PR   18-SEP-2000; 2000US-0233133P.
PR   18-SEP-2000; 2000US-0233617P.
PR   20-SEP-2000; 2000US-0234009P.
PR   20-SEP-2000; 2000US-0234034P.
PR   20-SEP-2000; 2000US-0234052P.
PR   22-SEP-2000; 2000US-0234509P.
PR   22-SEP-2000; 2000US-0234567P.
PR   25-SEP-2000; 2000US-0234923P.
PR   25-SEP-2000; 2000US-0234924P.
PR   25-SEP-2000; 2000US-0235077P.
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PR   25-SEP-2000; 2000US-0235082P.
PR   25-SEP-2000; 2000US-0235134P.
PR   25-SEP-2000; 2000US-0235280P.
PR   26-SEP-2000; 2000US-0235637P.
PR   26-SEP-2000; 2000US-0235638P.
PR   27-SEP-2000; 2000US-0235711P.
PR   27-SEP-2000; 2000US-0235720P.
PR   27-SEP-2000; 2000US-0235840P.
PR   27-SEP-2000; 2000US-0235863P.
PR   28-SEP-2000; 2000US-0236028P.
PR   28-SEP-2000; 2000US-0236032P.
PR   28-SEP-2000; 2000US-0236033P.
PR   28-SEP-2000; 2000US-0236034P.
PR   28-SEP-2000; 2000US-0236109P.
PR   28-SEP-2000; 2000US-0236111P.
PR   29-SEP-2000; 2000US-0236842P.
PR   29-SEP-2000; 2000US-0236891P.
PR   02-OCT-2000; 2000US-0237172P.
PR   02-OCT-2000; 2000US-0237173P.
PR   02-OCT-2000; 2000US-0237278P.
PR   02-OCT-2000; 2000US-0237294P.
PR   02-OCT-2000; 2000US-0237295P.
PR   02-OCT-2000; 2000US-0237316P.
PR   03-OCT-2000; 2000US-0237425P.
PR   03-OCT-2000; 2000US-0237598P.
PR   03-OCT-2000; 2000US-0237604P.
PR   03-OCT-2000; 2000US-0237606P.
PR   03-OCT-2000; 2000US-0237608P.
PR   01-NOV-2000; 2000US-0244867P.
PR   01-NOV-2000; 2000US-0245084P.
XX
PA   (AVAL-) AVALON PHARM.
XX
PI   Young PE,  Augustus M,  Carter KC,  Ebner R,  Endress G,  Horrigan S;
PI   Soppet DR,  Weaver Z;
XX
DR   WPI; 2002-188264/24.
DR   PC:NCBI; gi1318992.
XX
PT   Screening for anti-neoplastic agent involves exposing cells to a chemical
PT   agent to be tested for anti-neoplastic activity, and determining a change
PT   in expression of a gene of a signature gene set.
XX
PS   Claim 1; SEQ ID NO 3593; 44pp; English.
XX
CC   The present invention describes a method (M1) for screening for an anti-
CC   neoplastic agent. The method involves exposing cells to a chemical agent
CC   to be tested for anti-neoplastic activity, determining a change in
CC   expression of at least one gene (I) of a signature gene set, where (I)
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CC   comprises a sequence (S) selected from 8447 sequences (given in ABL61664
CC   to ABL70110), or is at least 95% identical to (S), where a change in
CC   expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC   activity and can be used in gene therapy. M1 can be used for screening an
CC   anti-neoplastic agent, and can be used for producing a product which is
CC   the data collected with respect to the anti-neoplastic agent as a result
CC   of M1, and the data is sufficient to convey the chemical structure and/or
CC   properties of the agent. M1 can be used in the treatment of cancer such
CC   as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,
CC   prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell
CC   cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous
CC   cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
CC   tumour
CC
CC   Revised record issued on 11-JUN-2007 : Enhanced with precomputed
CC   information from BOND.
XX
SQ   Sequence 574 BP; 140 A; 144 C; 158 G; 128 T; 0 U; 4 Other;

  Query Match             41.7%;  Score 367;  DB 1;  Length 574;
  Best Local Similarity   88.8%;  Pred. No. 8.3e-80;
  Matches  491;  Conservative    0;  Mismatches   42;  Indels   20;  Gaps    8;

Qy        348 GACAGGGTCGTGCCCAGATGATGGAGAAATCGACCCAGAAGCCTGAGGAGGTGTCCTGGG 407
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          7 GACAGGGTCGTGCCCAGATGATGGAGAAATCGACCCAGAAGCCTGAGGAGGTGTCCTGGG 66

Qy        408 TTTGGCTGGCTGGCTCCTGCTCCAGCGGCCCGGCTTCAGGTGTCCGGGGGCGTGGCTGCC 467
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 TTTGGCTGGCTGGCTCCTGCTCCAGCGGCCCGGCTTCAGGTGTCCGGGGGCGTGGCTGCC 126

Qy        468 TGGAGCAGGTGTGCTGAATACCCTGGATGGGAACTGAGCGAACCCGGGCCTCCGCTCAGA 527
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 TGGAGCAGGTGTGCTGAATACCCTGGATGGGAACTGAGCGAACCCGGGCCTCCGCTCAGA 186

Qy        528 GAGACGTGGCAGGACCAGCGAGGAATCCAGCCTGTCCACTTCCAGAACAGTGTTTCCCAG 587
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GAGACGTGGCAGGACCAGCGAGGAATCCAGCCTGTCCACTTCCAGAACAGTGTTTCCCAN 246

Qy        588 GCCCCGCTGAGTGGACCGGACCTCTGACACCTCC-AGGTTCTTGCTGACTCCGGCCTGGT 646
              |||||||| |||||||||||||||||||||||| |||||||||||||||||||||||||
Db        247 GCCCCGCTNAGTGGACCGGACCTCTGACACCTCCAAGGTTCTTGCTGACTCCGGCCTGGT 306

Qy        647 GAAAGGG-AGCGCCATGGTCCTGGCTGTTGGGGTCCCAGGGA--GAGGCTCTCTTCT-GG 702
              ||||||| ||||||||||||||||||||||||||||||||    |||||||||||| ||
Db        307 GAAAGGGAAGCGCCATGGTCCTGGCTGTTGGGGTCCCAGGGAAGAAGGCTCTCTTCTNGG 366

Qy        703 ACAAACACACCCTCCCAGCCCCCAGGGCTGT---GCAAACACATGCCCCTGCCATAAGCA 759
              |||||||||||||||||||||||||||||      | |||     ||| ||||||||
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Db        367 ACAAACACACCCTCCCAGCCCCCAGGGCTGTTGCAAACACATTGCCCCTTGCCATAAAGC 426

Qy        760 CCAACAAGAACTTCTTGCAGGTGGAGTG---------GCTGTTTTTTATAAGTTGTTTTA 810
                | | |  ||   |||    |  | |||         | | |||  || |  ||||||||
Db        427 ACCAAACAAAGAACTTCTTTGCAGGGTGGAGTGGGCTGTTTTTTAATAAAGTTTGTTTTA 486

Qy        811 CAGA-TACGGAAACAGTCCAAAATGGGATTTATAATTTCTTTTTT--GCATTATAAATAA 867
              |||| ||||||||||| |||||||||||||||||||||||||     | ||||||||
Db        487 CAGATTACGGAAACAGTTCAAAATGGGATTTATAATTTCTTTTTTTGCATTAATAAATAA 546

Qy        868 AGATCCTCTGTAA 880
              |||||||||||
Db        547 AGATCCTCTGTTA 559
```

RESULT 14
ADE07493
ID ADE07493 standard; DNA; 1617 BP.
XX
AC ADE07493;
XX
DT 29-JAN-2004 (first entry)
XX
DE Novel coding sequence (useful for identifying genetic disorders) #559.
XX
KW novel gene; novel protein; tissue marker; molecular weight marker;
KW chromosome marker; genetic disorder; gene; ds.
XX
OS Unidentified.
XX
PN WO2003054152-A2.
XX
PD 03-JUL-2003.
XX
PF 10-DEC-2002; 2002WO-US039555.
XX
PR 10-DEC-2001; 2001US-0339739P.
PR 11-DEC-2001; 2001US-0339453P.
PR 14-MAR-2002; 2002US-0365091P.
PR 14-MAR-2002; 2002US-0365384P.
PR 12-APR-2002; 2002US-0372381P.
PR 12-APR-2002; 2002US-0372615P.
PR 22-APR-2002; 2002US-00128558.
PR 24-APR-2002; 2002US-0376045P.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;
PI Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, Wang Z;

```
PI   Ma Y,  Wang D,  Chen R,  Xu C,  Boyle BJ;
XX
DR   WPI; 2003-569235/53.
DR   P-PSDB; ADE08404.
XX
PT   New polynucleotides, useful for expressing recombinant proteins for
PT   analysis, characterization or therapeutic use, or as markers for tissues
PT   in which the corresponding protein is preferentially expressed.
XX
PS   Claim 1; SEQ ID NO 559; 1177pp; English.
XX
CC   The invention comprises the amino acid and coding sequences of novel
CC   proteins. The DNA and protein sequences of the invention are useful as:
CC   markers for tissues in which the corresponding protein is preferentially
CC   expressed; as molecular weight markers on gels; as chromosome markers or
CC   tags; to identify chromosomes or to map related gene positions; and to
CC   compare with endogenous DNA sequences in patients to identify potential
CC   genetic disorders. The present DNA sequence represents a gene of the
CC   invention.
XX
SQ   Sequence 1617 BP; 374 A; 484 C; 474 G; 285 T; 0 U; 0 Other;

  Query Match             23.4%;  Score 206.4;  DB 1;  Length 1617;
  Best Local Similarity   99.5%;  Pred. No. 4.2e-40;
  Matches  207;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        186 GAAAGGCTTTCAAATGTGTGTCAGCAGCAGCAGCAGCAGCCACGACGAGGCCCCCGTCCT 245
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1410 GCAAGGCTTTCAAATGTGTGTCAGCAGCAGCAGCAGCAGCCACGACGAGGCCCCCGTCCT 1469

Qy        246 GAACGACAAGCACCTGGACGTGCCCGACATCATCATCACGCCCCCCACCCCCACGGGCAT 305
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1470 GAACGACAAGCACCTGGACGTGCCCGACATCATCATCACGCCCCCCACCCCCACGGGCAT 1529

Qy        306 GATGCTGCCGAGGGACTTGGGGAGCACAGTCTGGCTGGATGAGACAGGGTCGTGCCCAGA 365
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1530 GATGCTGCCGAGGGACTTGGGGAGCACAGTCTGGCTGGATGAGACAGGGTCGTGCCCAGA 1589

Qy        366 TGATGGAGAAATCGACCCAGAAGCCTGA 393
              |||||||||||||||||||||||||||||
Db       1590 TGATGGAGAAATCGACCCAGAAGCCTGA 1617


RESULT 15
AFS82561
ID   AFS82561 standard; DNA; 203 BP.
XX
AC   AFS82561;
XX
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DT   20-SEP-2007  (first entry)
XX
DE   Human transcript sequence, SEQ ID 1960.
XX
KW   DNA detection; RNA detection; exon; ds.
XX
OS   Homo sapiens.
XX
PN   WO200268579-A2.
XX
PD   06-SEP-2002.
XX
PF   10-JAN-2002; 2002WO-US000284.
XX
PR   10-JAN-2001; 2001US-00756696.
XX
PA   (PEKE ) PE CORP NY.
XX
PI   Venter CJ,  Adams M,  Li PWD,  Myers EW;
XX
DR   WPI; 2002-682812/73.
XX
PT   New isolated nucleic acid detection reagent for detecting the presence of
PT   specified human exons.
XX
PS   Claim 4; SEQ ID NO 1960; 40pp; English.
XX
CC   The present invention relates to a novel isolated nucleic acid detection
CC   reagent for detecting the presence of specified human exons. The exon
CC   sequences cover every identified human transcript and exon comprising
CC   every gene/coding region of the human genome. The present sequence is one
CC   such exon sequence. The nucleic acid detection agent is used for
CC   detecting the presence of at least 100000, at least 2000, at least 50000
CC   or at least 10000 human exons. The sequences that span exon-exon
CC   junctions eliminate false signals caused by genomic contamination. This
CC   is because a detection element comprising two neighboring exons as one
CC   contiguous sequence will not hybridize to genomic DNA comprising
CC   intervening intronic DNA. These detection elements will only hybridize to
CC   expressed mRNA transcripts in which the exons are connected and the
CC   intronic sequence has been removed, therefore forming one contiguous
CC   stretch of sequence corresponding to the sequence of the detection
CC   element that spans the exon-exon junction.
XX
SQ   Sequence 203 BP; 49 A; 65 C; 60 G; 29 T; 0 U; 0 Other;

  Query Match             23.0%;  Score 203;  DB 1;  Length 203;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-39;
  Matches  203;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy        191 GCTTTCAAATGTGTGTCAGCAGCAGCAGCAGCAGCCACGACGAGGCCCCCGTCCTGAACG 250
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GCTTTCAAATGTGTGTCAGCAGCAGCAGCAGCAGCCACGACGAGGCCCCCGTCCTGAACG 60

Qy        251 ACAAGCACCTGGACGTGCCCGACATCATCATCACGCCCCCCACCCCCACGGGCATGATGC 310
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACAAGCACCTGGACGTGCCCGACATCATCATCACGCCCCCCACCCCCACGGGCATGATGC 120

Qy        311 TGCCGAGGGACTTGGGGAGCACAGTCTGGCTGGATGAGACAGGGTCGTGCCCAGATGATG 370
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TGCCGAGGGACTTGGGGAGCACAGTCTGGCTGGATGAGACAGGGTCGTGCCCAGATGATG 180

Qy        371 GAGAAATCGACCCAGAAGCCTGA 393
              |||||||||||||||||||||||
Db        181 GAGAAATCGACCCAGAAGCCTGA 203


Search completed: April 28, 2009, 04:16:11
Job time : 236 secs
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SCORE 3.0